



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/552,786

DATE: 10/24/2005

TIME: 10:49:40

Input Set : A:\SEQLIST.txt
 Output Set: N:\CRF4\10242005\J552786.raw

5 <110> APPLICANT: DEPERTHES, David
 6 CLOUTIER, Sylvain
 9 <120> TITLE OF INVENTION: Inhibitor proteins of a protease and use thereof
 12 <130> FILE REFERENCE: KZI-003US
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/552,786
C--> 15 <141> CURRENT FILING DATE: 2005-10-03
 15 <150> PRIOR APPLICATION NUMBER: PCT/IB2004/001040
 16 <151> PRIOR FILING DATE: 2004-04-05
 19 <150> PRIOR APPLICATION NUMBER: US 60/460345
 20 <151> PRIOR FILING DATE: 2003-04-04
 24 <160> NUMBER OF SEQ ID NOS: 22
 28 <170> SOFTWARE: PatentIn version 3.1
 32 <210> SEQ ID NO: 1
 34 <211> LENGTH: 1239
 36 <212> TYPE: DNA
 38 <213> ORGANISM: Artificial sequence
 42 <220> FEATURE:
 44 <223> OTHER INFORMATION: DNA Sequence ACT variants : MD 820
 46 <400> SEQUENCE: 1
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 51 gccaacgtgg acttcgttt cagcctgtac aagcgttag tcctgaaggc ccctgataag 180
 53 aatgtcatct tctccccact gacatctcc accgccttgg ctttcctgtc tctggggcc 240
 55 cataatacca ccctgacaga gattctcaaa ggcctcaagt tcaacctcac ggagacttct 300
 57 gaggcagaaa ttccaccagag ctcccagcac ctccctgcga ccctcaatca gtccagcgat 360
 59 gagctgcgc tgagtatggg aaatgccatg tttgtcaaag agcaactca tagtgcgtggac 420
 61 aggttcacgg aggatgccaa gaggctgtat ggctccgagg ctttgccac tgactttcag 480
 63 gactcagctg cagctaagaa gctcatcaac gactacgtga agaatggAAC tagggggAAA 540
 65 atcacagato tcatcaagga ccttgactcg cagacaatga tggctctgtt gaattacatc 600
 67 ttctttaaag ccaaattgggA gatgccctt gaccccaAG atactcatca gtcaaggTTc 660
 69 tacttgagca agaaaaAGTg ggtaatggTG cccatgatga gtttgcatca cctgactata 720
 71 ccttaactcc gggacgagga gctgtcctgc accgtgggtt agctgaagta cacaggcaat 780
 73 gccagcgcac tcttcatect ccctgatcaa gacaagatgg aggaagtgg agccatgctg 840
 75 ctccccagaga ccctgaagcg gtggagagac tctctggagt tcagagagat aggtgagctc 900
 77 tacctgccaa agtttccat ctcgaggAAC tataacctga acgacataact tctccagctg 960
 79 ggcattgagg aagccttcac cagcaaggct gacctgtcag ggatcacagg ggcaggAAC 1020
 81 ctagcagtct cccaggtggt ccataaggct gtgctgtat tatttgagGA gggcacAGAA 1080
 83 gcatctgctg ccaccgcggT caaaatcacc ctccgttctc gacgtggA gacgcgtacc 1140
 85 attgtgcgtt tcaacaggCC cttcctgtat atcatgtcc ctacagacac ccagaacatc 1200
 87 ttcttcatga gcaaagtcaC caatcccaAG caagcctaa 1239
 90 <210> SEQ ID NO: 2
 92 <211> LENGTH: 412
 94 <212> TYPE: PRT

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96 <213> ORGANISM: Artificial sequence
 100 <220> FEATURE:
 102 <223> OTHER INFORMATION: Protein Sequence ACT variants : MD 820
 104 <400> SEQUENCE: 2
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 107 1 5 10 15
 110 Pro Leu Asp Glu Glu Asn Leu Thr Gln Glu Asn Gln Asp Arg Gly Thr
 111 20 25 30
 114 His Val Asp Leu Gly Leu Ala Ser Ala Asn Val Asp Phe Ala Phe Ser
 115 35 40 45
 118 Leu Tyr Lys Gln Leu Val Leu Lys Ala Pro Asp Lys Asn Val Ile Phe
 119 50 55 60
 122 Ser Pro Leu Ser Ile Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala
 123 65 70 75 80
 126 His Asn Thr Thr Leu Thr Glu Ile Leu Lys Gly Leu Lys Phe Asn Leu
 127 85 90 95
 130 Thr Glu Thr Ser Glu Ala Glu Ile His Gln Ser Phe Gln His Leu Leu
 131 100 105 110
 134 Arg Thr Leu Asn Gln Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn
 135 115 120 125
 138 Ala Met Phe Val Lys Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu
 139 130 135 140
 142 Asp Ala Lys Arg Leu Tyr Gly Ser Glu Ala Phe Ala Thr Asp Phe Gln
 143 145 150 155 160
 146 Asp Ser Ala Ala Ala Lys Lys Leu Ile Asn Asp Tyr Val Lys Asn Gly
 147 165 170 175
 150 Thr Arg Gly Lys Ile Thr Asp Leu Ile Lys Asp Leu Asp Ser Gln Thr
 151 180 185 190
 154 Met Met Val Leu Val Asn Tyr Ile Phe Phe Lys Ala Lys Trp Glu Met
 155 195 200 205
 158 Pro Phe Asp Pro Gln Asp Thr His Gln Ser Arg Phe Tyr Leu Ser Lys
 159 210 215 220
 162 Lys Lys Trp Val Met Val Pro Met Met Ser Leu His His Leu Thr Ile
 163 225 230 235 240
 166 Pro Tyr Phe Arg Asp Glu Glu Leu Ser Cys Thr Val Val Glu Leu Lys
 167 245 250 255
 170 Tyr Thr Gly Asn Ala Ser Ala Leu Phe Ile Leu Pro Asp Gln Asp Lys
 171 260 265 270
 174 Met Glu Glu Val Glu Ala Met Leu Leu Pro Glu Thr Leu Lys Arg Trp
 175 275 280 285
 178 Arg Asp Ser Leu Glu Phe Arg Glu Ile Gly Glu Leu Tyr Leu Pro Lys
 179 290 295 300
 182 Phe Ser Ile Ser Arg Asp Tyr Asn Leu Asn Asp Ile Leu Leu Gln Leu
 183 305 310 315 320
 186 Gly Ile Glu Glu Ala Phe Thr Ser Lys Ala Asp Leu Ser Gly Ile Thr
 187 325 330 335
 190 Gly Ala Arg Asn Leu Ala Val Ser Gln Val Val His Lys Ala Val Leu
 191 340 345 350
 194 Asp Val Phe Glu Glu Gly Thr Glu Ala Ser Ala Ala Thr Ala Val Lys

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195	355	360	365
198	Ile Thr Leu Arg Ser Arg Ala Val Glu Thr Arg Thr Ile Val Arg Phe		
199	370	375	380
202	Asn Arg Pro Phe Leu Met Ile Ile Val Pro Thr Asp Thr Gln Asn Ile		
203	385	390	395
206	Phe Phe Met Ser Lys Val Thr Asn Pro Lys Gln Ala		400
207	405	410	
210	<210> SEQ ID NO: 3		
212	<211> LENGTH: 1239		
214	<212> TYPE: DNA		
216	<213> ORGANISM: Artificial sequence		
220	<220> FEATURE:		
222	<223> OTHER INFORMATION: DNA Sequence ACT variant : MD 62		
224	<400> SEQUENCE: 3		
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227	gagaatctga cccaggagaa ccaagaccga gggacacacg tggacctcg attagcctcc	120	
229	gccaacgtgg acttcgttt cagcgtac aagcagttag tcctgaaggc ccctgataag	180	
231	aatgtcatct tctccccact gagcatctcc accgcottgg ccttcctgtc tctggggcc	240	
233	cataatacca ccctgacaga gattctaaa ggcctaagt tcaacctcac ggagacttct	300	
235	gaggcagaaa ttcaccagag cttccagcac ctccctgc ccctcaatca gtccagcgat	360	
237	gagctgcagc tgagtatggg aaatgccatg tttgtcaaag agcaactcag tctgctggac	420	
239	aggttcacgg aggatgcca gaggctgtat ggctccgagg ccttgcac tgactttcag	480	
241	gactcagctg cagctaagaa gctcatcaac gactacgtga agaatggAAC tagggggAAA	540	
243	atcacagatc tgatcaagga cttgactcg cagacaatga tggctctgggt gaattacatc	600	
245	ttctttaag ccaaattgggat gatgccctt gaccccaag atactcatca gtcaagggttc	660	
247	tacttgagca agaaaaagtgt gtaatgggt cccatgtga gtttgcata cctgactata	720	
249	ccttacttcc gggacgagga gctgtcctgc accgtgggt agctgaagta cacaggcaat	780	
251	gccagcgcac tcttcatcct ccctgatcaa gacaagatgg aggaagtgg agccatgctg	840	
253	ctcccagaga ccctgaagcg gtggagagac tctctggagt tcagagagat aggtgagctc	900	
255	tacctgccaa agtttccat ctgcaggagataaacctga acgacataact tctccagctg	960	
257	ggcattgagg aagccttcac cagcaaggct gacctgttag gatatcacagg ggccagggAAC	1020	
259	ctagcagtct cccaggtggt ccataaggct gtgcgtatg tatttgaggg gggcacagaa	1080	
261	gcatctgtcg ccaccgcggtaaaaatcacc aggaggctta tcgcgttggaa gacgcgtacc	1140	
263	attgtgcgtt tcaacaggcc cttcctgtatg atcattgtcc ctacagacac ccagaacatc	1200	
265	ttcttcatga gcaaagtca caatccaaag caagcctaa	1239	
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274	<213> ORGANISM: Artificial sequence		
278	<220> FEATURE:		
280	<223> OTHER INFORMATION: Protein Sequence ACT variant : MD 62		
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285	1 5 10 15		
288	Pro Leu Asp Glu Glu Asn Leu Thr Gln Glu Asn Gln Asp Arg Gly Thr		
289	20 25 30		
292	His Val Asp Leu Gly Leu Ala Ser Ala Asn Val Asp Phe Ala Phe Ser		
293	35 40 45		
296	Leu Tyr Lys Gln Leu Val Leu Lys Ala Pro Asp Lys Asn Val Ile Phe		

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297	50	55	60
300	Ser Pro Leu Ser Ile Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala		
301	65	70	75
304	His Asn Thr Thr Leu Thr Glu Ile Leu Lys Gly Leu Lys Phe Asn Leu		80
305	85	90	95
308	Thr Glu Thr Ser Glu Ala Glu Ile His Gln Ser Phe Gln His Leu Leu		
309	100	105	110
312	Arg Thr Leu Asn Gln Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn		
313	115	120	125
316	Ala Met Phe Val Lys Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu		
317	130	135	140
320	Asp Ala Lys Arg Leu Tyr Gly Ser Glu Ala Phe Ala Thr Asp Phe Gln		
321	145	150	155
324	Asp Ser Ala Ala Ala Lys Lys Leu Ile Asn Asp Tyr Val Lys Asn Gly		160
325	165	170	175
328	Thr Arg Gly Lys Ile Thr Asp Leu Ile Lys Asp Leu Asp Ser Gln Thr		
329	180	185	190
332	Met Met Val Leu Val Asn Tyr Ile Phe Phe Lys Ala Lys Trp Glu Met		
333	195	200	205
336	Pro Phe Asp Pro Gln Asp Thr His Gln Ser Arg Phe Tyr Leu Ser Lys		
337	210	215	220
340	Lys Lys Trp Val Met Val Pro Met Met Ser Leu His His Leu Thr Ile		
341	225	230	235
344	Pro Tyr Phe Arg Asp Glu Glu Leu Ser Cys Thr Val Val Glu Leu Lys		240
345	245	250	255
348	Tyr Thr Gly Asn Ala Ser Ala Leu Phe Ile Leu Pro Asp Gln Asp Lys		
349	260	265	270
352	Met Glu Glu Val Glu Ala Met Leu Leu Pro Glu Thr Leu Lys Arg Trp		
353	275	280	285
356	Arg Asp Ser Leu Glu Phe Arg Glu Ile Gly Glu Leu Tyr Leu Pro Lys		
357	290	295	300
360	Phe Ser Ile Ser Arg Asp Tyr Asn Leu Asn Asp Ile Leu Leu Gln Leu		
361	305	310	315
364	Gly Ile Glu Glu Ala Phe Thr Ser Lys Ala Asp Leu Ser Gly Ile Thr		320
365	325	330	335
368	Gly Ala Arg Asn Leu Ala Val Ser Gln Val Val His Lys Ala Val Leu		
369	340	345	350
372	Asp Val Phe Glu Glu Gly Thr Glu Ala Ser Ala Ala Thr Ala Val Lys		
373	355	360	365
376	Ile Thr Arg Arg Ser Ile Asp Val Glu Thr Arg Thr Ile Val Arg Phe		
377	370	375	380
380	Asn Arg Pro Phe Leu Met Ile Ile Val Pro Thr Asp Thr Gln Asn Ile		
381	385	390	395
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388	<210> SEQ ID NO: 5		
390	<211> LENGTH: 1239		
392	<212> TYPE: DNA		
394	<213> ORGANISM: Artificial sequence		

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Output Set: N:\CRF4\10242005\J552786.raw

398 <220> FEATURE:

400 <223> OTHER INFORMATION: DNA Sequence ACT variant : MD 83

402 <400> SEQUENCE: 5

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407 gccaacgtgg	acttgcgttt	cagcctgtac	aagcagttag	tcctgaaggc	ccctgataag	180
409 aatgtcatct	tctccccact	gagcatctcc	accgccttgg	ccttcctgtc	tctgggggcc	240
411 cataataccca	ccctgacaga	gattctcaaa	ggcctcaagt	tcaacctcac	ggagacttct	300
413 gaggcagaaa	ttcaccagag	cttccagcac	ctccctgcgc	ccctcaatca	gtccagcgt	360
415 gagctgcagc	tgagtatggg	aatgccatg	tttgtcaaag	agcaactcag	tctgctggac	420
417 aggttcacgg	aggatgccaa	gaggctgtat	ggctccgagg	cctttgcac	tgactttcag	480
419 gactcagctg	cagctaagaa	gctcatcaac	gactacgtga	agaatgaaac	tagggggaaa	540
421 atcacagatc	tgatcaagga	ccttgactcg	cagacaatga	tggtcctgtt	gaattacatc	600
423 ttctttaaag	ccaaatggga	gatgccctt	gaccggcaag	ataactcatca	gtcaaggttc	660
425 tacttgagca	agaaaaagtg	ggttatggtg	cccatgatga	gtttgcatca	cctgactata	720
427 ccttacttcc	gggacgagga	gctgtcctgc	accgtgggtgg	agctgaagta	cacaggcaat	780
429 gccagcgcac	tcttcatcct	ccctgatcaa	gacaagatgg	aggaagtgg	agccatgctg	840
431 ctcccagaga	ccctgaagcg	gtggagagac	tctctggagt	tcagagagat	agtgagctc	900
433 tacctgccaa	agtttccat	ctcgagggac	tataacctga	acgacatact	tctccagctg	960
435 ggcattgagg	aagccttcac	cagcaaggct	gacctgtcag	ggatcacagg	ggccaggaac	1020
437 ctagcagtct	cccaggtgg	ccataaggct	gtgcttgatg	tatggagga	gggcacagaa	1080
439 gcatctgctg	ccaccgcgg	caaaatcagg	gggagatctg	agtttagtgg	gacgcgtacc	1140
441 attgtgcgtt	tcaacaggcc	cttcctgtat	atcattgtcc	ctacagacac	ccagaacatc	1200
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448 <211> LENGTH: 412

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452 <213> ORGANISM: Artificial sequence

456 <220> FEATURE:

458 <223> OTHER INFORMATION: Protein Sequence ACT variant : MD 83

460 <400> SEQUENCE: 6

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467				20			25				30				
470 His	Val	Asp	Leu	Gly	Leu	Ala	Ser	Ala	Asn	Val	Asp	Phe	Ala	Phe	Ser
471				35			40				45				
474 Leu	Tyr	Lys	Gln	Leu	Val	Leu	Lys	Ala	Pro	Asp	Lys	Asn	Val	Ile	Phe
475				50			55				60				
478 Ser	Pro	Leu	Ser	Ile	Ser	Thr	Ala	Leu	Ala	Phe	Leu	Ser	Leu	Gly	Ala
479				65			70				75				80
482 His	Asn	Thr	Thr	Leu	Thr	Glu	Ile	Leu	Lys	Gly	Leu	Lys	Phe	Asn	Leu
483				85			90				95				
486 Thr	Glu	Thr	Ser	Glu	Ala	Glu	Ile	His	Gln	Ser	Phe	Gln	His	Leu	Leu
487				100			105				110				
490 Arg	Thr	Leu	Asn	Gln	Ser	Ser	Asp	Glu	Leu	Gln	Leu	Ser	Met	Gly	Asn
491				115			120				125				
494 Ala	Met	Phe	Val	Lys	Glu	Gln	Leu	Ser	Leu	Leu	Asp	Arg	Phe	Thr	Glu
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VERIFICATION SUMMARY

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L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1004 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:1000